

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Kaushansky, Kenneth
- (ii) TITLE OF INVENTION: Methods of Stimulating Erythropoiesis  
Using Hematopoietic Proteins.
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: ZymoGenetics, Inc.
  - (B) STREET: 1201 Eastlake Avenue East
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98102
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Parker, Gary E
  - (B) REGISTRATION NUMBER: 31-648
  - (C) REFERENCE/DOCKET NUMBER: 94-09C2
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 206-442-6673
  - (B) TELEFAX: 206-442-6678

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA	48
Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala	
1 5 10 15	
AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC	96
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val	
20 25 30	
CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC	144
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser	
35 40 45	
CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT	192
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala	
50 55 60	
GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG	240
Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys	
65 70 75 80	
GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG	288
Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met	
85 90 95	
GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG	336
Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly	
100 105 110	
CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC	384
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu	
115 120 125	

CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp 130 135 140	432
CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val 145 150 155 160	480
CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala 165 170 175	528
CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu 180 185 190	576
AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr 195 200 205	624
GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly 210 215 220	672
TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu 225 230 235 240	720
GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly 245 250 255	768
ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro 260 265 270	816
GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu 275 280 285	864
CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr 290 295 300	912

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Thr	Glu	Leu	Leu	Leu	Val	Val	Met	Leu	Leu	Leu	Thr	Ala
1				5					10					15	
Arg	Leu	Thr	Leu	Ser	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val
			20					25					30		
Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser
		35					40					45			
Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala
	50					55					60				
Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys
65					70					75					80
Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
				85					90					95	

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
 100 105 110

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
 115 120 125

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
 130 135 140

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 145 150 155 160

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
 165 170 175

Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
 180 185 190

Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
 195 200 205

Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
 210 215 220

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
 225 230 235 240

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
 245 250 255

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
 260 265 270

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
 275 280 285

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
 290 295 300

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
 305 310 315 320

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
 325 330 335

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
                   340                  345                  350

Gly

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 1081

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105..1241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTCGTGCCG GTCCTGAGGC CTTCTCCAC CCGACAGAG TCCTTGCCCC ACCTCTCTCC	60
CACCCGACTC TGCCGAAAGA AGCACAGAAG CTCAAGCCGC CTCC ATG GCC CCA GGA	116
Met Ala Pro Gly	
1	
AAG ATT CAG GGG AGA GGC CCC ATA CAG GGA GCC ACT TCA GTT AGA CAC	164
Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr Ser Val Arg His	
5                  10                  15                  20	
CTG GCC AGA ATG GAG CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT	212
Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu	
25                  30                  35	
GCA GTG GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT GAC	260
Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp	
40                  45                  50	

CCC	AGA	CTC	CTA	AAT	AAA	CTG	CTG	CGT	GAC	TCC	CAC	CTC	CTT	CAC	AGC	308
Pro	Arg	Leu	Leu	Asn	Lys	Leu	Leu	Arg	Asp	Ser	His	Leu	Leu	His	Ser	
		55					60					65				
CGA	CTG	AGT	CAG	TGT	CCC	GAC	GTC	GAC	CCT	TTG	TCT	ATC	CCT	GTT	CTG	356
Arg	Leu	Ser	Gln	Cys	Pro	Asp	Val	Asp	Pro	Leu	Ser	Ile	Pro	Val	Leu	
	70					75				80						
CTG	CCT	GCT	GTG	GAC	TTT	AGC	CTG	GGA	GAA	TGG	AAA	ACC	CAG	ACG	GAA	404
Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Thr	Glu	
85					90				95						100	
CAG	AGC	AAG	GCA	CAG	GAC	ATT	CTA	GGG	GCA	GTG	TCC	CTT	CTA	CTG	GAG	452
Gln	Ser	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Ser	Leu	Leu	Leu	Glu	
			105					110						115		
GGA	GTG	ATG	GCA	GCA	CGA	GGA	CAG	TTG	GAA	CCC	TCC	TGC	CTC	TCA	TCC	500
Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	
		120					125						130			
CTC	CTG	GGA	CAG	CTT	TCT	GGG	CAG	GTT	CGC	CTC	CTC	TTG	GGG	GCC	CTG	548
Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	
		135				140						145				
CAG	GGC	CTC	CTA	GGA	ACC	CAG	CTT	CCT	CTA	CAG	GGC	AGG	ACC	ACA	GCT	596
Gln	Gly	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Leu	Gln	Gly	Arg	Thr	Thr	Ala	
	150					155				160						
CAC	AAG	GAC	CCC	AAT	GCC	CTC	TTC	TTG	AGC	TTG	CAA	CAA	CTG	CTT	CGG	644
His	Lys	Asp	Pro	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu	Arg	
165					170				175						180	
GGA	AAG	GTG	CGC	TTC	CTG	CTT	CTG	GTA	GAA	GGT	CCC	ACC	CTC	TGT	GTC	692
Gly	Lys	Val	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	
			185					190						195		
AGA	CGG	ACC	CTG	CCA	ACC	ACA	GCT	GTC	CCA	AGC	AGT	ACT	TCT	CAA	CTC	740
Arg	Arg	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	Leu	
		200					205						210			
CTC	ACA	CTA	AAC	AAG	TTC	CCA	AAC	AGG	ACT	TCT	GGA	TTG	TTG	GAG	ACG	788
Leu	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	
	215					220					225					

AAC TTC AGT GTC ACA GCC AGA ACT GCT GGC CCT GGA CTT CTG AGC AGG Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg 230 235 240	836
CTT CAG GGA TTC AGA GTC AAG ATT ACT CCT GGT CAG CTA AAT CAA ACC Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr 245 250 255 260	884
TCC AGG TCC CCA GTC CAA ATC TCT GGA TAC CTG AAC AGG ACA CAC GGA Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly 265 270 275	932
CCT GTG AAT GGA ACT CAT GGG CTC TTT GCT GGA ACC TCA CTT CAG ACC Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr 280 285 290	980
CTG GAA GCC TCA GAC ATC TCG CCC GGA GCT TTC AAC AAA GGC TCC CTG Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu 295 300 305	1028
GCA TTC AAC CTC CAG GGT GGA CTT CCT CCT TCT CCA AGC CTT GCT CCT Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro 310 315 320	1076
GAT GGA CAC ACA CCC TTC CCT CCT TCA CCT GCC TTG CCC ACC ACC CAT Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His 325 330 335 340	1124
GGA TCT CCA CCC CAG CTC CAC CCC CTG TTT CCT GAC CCT TCC ACC ACC Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr 345 350 355	1172
ATG CCT AAC TCT ACC GCC CCT CAT CCA GTC ACA ATG TAC CCT CAT CCC Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro 360 365 370	1220
AGG AAT TTG TCT CAG GAA ACA TAGCGCGGGC ACTGGCCCAG TGAGCGTCTG Arg Asn Leu Ser Gln Glu Thr 375	1271
CAGCTTCTCT CGGGGACAAG CTTCCCCAGG AAGGCTGAGA GGCAGCTGCA TCTGCTCCAG	1331
ATGTTCTGCT TTCACCTAAA AGGCCCTGGG GAAGGGATAC ACAGCACTGG AGATTGTAAA	1391



ATTTTAGGAG CTATTTTTTT TTAACCTATC AGCAATATTC ATCAGAGCAG CTAGCGATCT 1451

TTGGTCTATT TTCGGTATAA ATTTGAAAAT CACTA 1486

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Gly Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr  
1 5 10 15

Ser Val Arg His Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala  
20 25 30

Ala Met Leu Leu Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala  
35 40 45

Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His  
50 55 60

Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser  
65 70 75 80

Ile Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys  
85 90 95

Thr Gln Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser  
100 105 110

Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser  
115 120 125

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu  
130 135 140

Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly  
 145 150 155 160  
 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln  
 165 170 175  
 Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro  
 180 185 190  
 Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser  
 195 200 205  
 Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly  
 210 215 220  
 Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly  
 225 230 235 240  
 Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln  
 245 250 255  
 Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn  
 260 265 270  
 Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr  
 275 280 285  
 Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn  
 290 295 300  
 Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro  
 305 310 315 320  
 Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu  
 325 330 335  
 Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp  
 340 345 350  
 Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met  
 355 360 365  
 Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr  
 370 375

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(632..644, 876..1003, 1290..1376, 3309..3476, 3713..4375)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CTTTCTTGCT TTCTTTCTTT CTTTCTTTCT TTCTTTTTTT TTTTGAGAC GGAGTTTCAC      60
TCTTATTGCC CAGGCTGGAG TGCAATGGTG CGATCTCGGC TCACCACAAC CTCCGCCTCC      120
CAGGTACAAG CGATTCTCCT GTCTCAGCCT CCCAAGTAGC TTGGATTACA GGCATGAACC      180
ACCACACCCT GCTAGTTTTT TTGTATTTCT TAGAGCCGGG GTTTCACCAT GTTAGTGAGG      240
CTGGTGGCGA ACTCCTGACC TCAGGTGATC CACCCGCCTT GGA CTCCCAA AGTGCTGGGA      300
TTACAGGCAT GAGCCACTGC ACCCGGCACA CCATATGCTT TCATCACAAG AAAATGTGAG      360
AGAATTCAGG GCTTTGGCAG TTCCAGGCTG GTCAGCATCT CAAGCCCTCC CCAGCATCTG      420
TTCACCCTGC CAGGCAGTCT CTTCTAGAA ACTTGGTTAA ATGTTCACTC TTCTTGCTAC      480
TTTCAGGATA GATTCTTCAC CTTGGTCCG CCTTTGCCCC ACCCTACTCT GCCCAGAAGT      540
GCAAGAGCCT AAGCCGCCTC CATGGCCCCA GGAAGGATTC AGGGGAGAGG CCCCAAACAG      600
GGAGCCACGC CAGCCAGACA CCCCAGCCAG A ATG GAG CTG ACT  G GTGAGAACAC      654
                               Met Glu Leu Thr
                               1
ACCTGAGGGG CTAGGGCCAT ATGGAAACAT GACAGAAGGG GAGAGAGAAA GGAGACACGC      714

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TGCAGGGGGC AGGAAGCTGG GGAACCCAT TCTCCCAAAA ATAAGGGGTC TGAGGGGTGG	774
ATTCCTGGG TTTCAGGTCT GGGTCCTGAA TGGAATTCC TGAATACCA GCTGACAATG	834
ATTCCTCCT CATCTTTCAA CCTCACCTCT CCTCATCTAA G AA TTG CTC CTC Glu Leu Leu Leu 5	886
GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala 10 15 20	934
CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser 25 30 35 40	982
CAT GTC CTT CAC AGC AGA CTG GTGAGAACTC CCAACATTAT CCCCTTTATC His Val Leu His Ser Arg Leu 45	1033
CGCGTAACTG GTAAGACACC CATACTCCCA GGAAGACACC ATCACTTCCT CTAATCCTT	1093
GACCCAATGA CTATTCTTCC CATATTGTCC CCACCTACTG ATCACACTCT CTGACAAGGA	1153
TTATTCTTCA CAATACAGCC CGCATTTAAA AGCTCTCGTC TAGAGATAGT ACTCATGGAG	1213
GACTAGCCTG CTTATTAGGC TACCATAGCT CTCTCTATTT CAGCTCCCTT CTCCCCCACC	1273
CAATCTTTTT CAACAG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr 50 55	1322
CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr 60 65 70	1370
CAG ATG GTAAGAAAGC CATCCCTAAC CTTGGCTTCC CTAAGTCCTG TCTTCAGTTT Gln Met 75	1426
CCCACTGCTT CCCATGGATT CTCCAACATT CTTGAGCTTT TAAAAAATAT CTCACCTTCA	1486
GCTTGGCCAC CCTAACCCAA TCTACATTCA CCTATGATGA TAGCCTGTGG ATAAGATGAT	1546
GGCTTGCAGG TCCAATATGT GAATAGATTT GAAGCTGAAC ACCATGAAAA GCTGGAGAGA	1606

AATCGCTCAT GGCCATGCCT TTGACCTATT CCCGTTTCAGT CTTCTTAAAT TGGCATGAAG	1666
AAGCAAGACT CATATGTCAT CCACAGATGA CACAAAGCTG GGAAGTACCA CTAAAATAAC	1726
AAAAGACTGA ATCAAGATTC AAATCACTGA AAGACTAGGT CAAAAACAAG GTGAAACAAC	1786
AGAGATATAA ACTTCTACAT GTGGGCCGGG GGCTCACGCC TGTAATCCCA GCACTTTGGG	1846
AGGCCGAGGC AGGCAGATCA CCTGAGGGCA GGAGTTTGAG AGCAGCCTGG CCAACATGGC	1906
GAAACCCCGT CTCTACTAAG AATACAGAAT TAGCCGGGCA TGGTAGTGCA TGCCTGTAAT	1966
CCCAGCTACT TGAAGGCTG AAGCAGGAGA ATCCCTTGAA CCCAGGAGGT GGAGGTTGTA	2026
GTGAGCTGAG ATCATGCCAA TGCACTCCAG CCTGGGTGAC AAGAGCAAAA CTCCTCTCA	2086
AAAAGAAAAA AAAATTCTAC ATGTGTAAAT TAATGAGTAA AGTCCTATTC CAGCTTTCAG	2146
GCCACAATGC CCTGCTTCCA TCATTAAAGC CTCTGGCCCT AGCACTTCCT ACGAAAAGGA	2206
TCTGAGAGAA TTAAATTGCC CCCAACTTA CCATGTAACA TTAAGTGAAGC TGCTATTCTT	2266
AAAGCTAGTA ATTCTTGTCT GTTTGATGTT TAGCATCCCC ATTGTGGAAA TGCTCGTACA	2326
GAAGCTCTATT CCGAGTGGAC TACACTTAAA TATACTGGCC TGAACACCGG ACATCCCCCT	2386
GAAGACATAT GCTAATTTAT TAAGAGGGAC CATATTAAAC TAACATGTGT CTAGAAAGCA	2446
GCAGCCTGAA CAGAAAGAGA CTAGAAGCAT GTTTTATGGG CAATAGTTTA AAAAATAAAA	2506
ATCTATCCTC AAGAACCCTA GCGTCCCTTC TTCCTTCAGG ACTGAGTCAG GGAAGAAGGG	2566
CAGTTCCTAT GGGTCCCTTC TAGTCCTTTC TTTTCATCCT TATGATCATT ATGGTAGAGT	2626
CTCATACCTA CATTTAGTTT ATTTATTATT ATTATTTGAG ACGGAGTCTC ACTCTATCCC	2686
CCAGGCTGGA GTGCAGTGGC ATGATCTCAA CTCAGTCAA CCTCAGCCTC CCGGATTCAA	2746
GCGATTCTCC TGTCTCAGTC TCCCAAGTAG CTGGGATTAC AGGTGCCCAC CACCATGCCC	2806
AGCTAATTTG TGTATTTGTG GTAGAGATGG GGTTTCACCA TGTGAGGAG GCTGATCTTG	2866
AACTCCTGAC CTCAGGTGAT CCACCTGCCT CAGCCTCCCA AAGTGCTGGG ATTACAGGCG	2926

TGAGCCACTG CACCCAGCCT TCATTCAAGT TAAAAATCAA ATGATCCTAA GGTTTTGCAG	2986
CAGAAAGAGT AAATTTGCAG CACTAGAACC AAGAGGTAAA AGCTGTAACA GGGCAGATTT	3046
CAGCAACGTA AGAAAAAAGG AGCTCTTCTC ACTGAAACCA AGTGTAAGAC CAGGCTGGAC	3106
TAGAGGACAC GGGAGTTTTT GAAGCAGAGG CTGATGACCA GCTGTCGGGA GACTGTGAAG	3166
GAATTCCTGC CCTGGGTGGG ACCTTGGTCC TGTCCAGTTC TCAGCCTGTA TGATTCATC	3226
TGCTGGCTAC TCCTAAGGCT CCCACCCGC TTTTAGTGTG CCCTTTGAGG CAGTGCCTT	3286
CTCTCTTCCA TCTCTTTCTC AG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA	3338
Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly	
80 85	
GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG	3386
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu	
90 95 100	
GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC	3434
Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val	
105 110 115	
CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG	3476
Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln	
120 125 130	
GTAAGTCCCC AGTCAAGGGA TCTGTAGAAA CTGTTCTTTT CTGACTCAGT CCCCTAGAA	3536
GACCTGAGGG AAGAAGGGCT CTTCCAGGGA GCTCAAGGGC AGAAGAGCTG ATCTACTAAG	3596
AGTGCTCCCT GCCAGCCACA ATGCCTGGGT ACTGGCATCC TGTCTTTCCT ACTTAGACAA	3656
GGGAGGCCTG AGATCTGGCC CTGGTGTTTG GCCTCAGGAC CATCCTCTGC CCTCAG	3712
CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC	3760
Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile	
135 140 145	
TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG	3808
Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met	
150 155 160	

CTT	GTA	GGA	GGG	TCC	ACC	CTC	TGC	GTC	AGG	CGG	GCC	CCA	CCC	ACC	ACA	3856
Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	
165					170				175						180	
GCT	GTC	CCC	AGC	AGA	ACC	TCT	CTA	GTC	CTC	ACA	CTG	AAC	GAG	CTC	CCA	3904
Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	
				185					190					195		
AAC	AGG	ACT	TCT	GGA	TTG	TTG	GAG	ACA	AAC	TTC	ACT	GCC	TCA	GCC	AGA	3952
Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	
			200					205					210			
ACT	ACT	GGC	TCT	GGG	CTT	CTG	AAG	TGG	CAG	CAG	GGA	TTC	AGA	GCC	AAG	4000
Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	
		215					220					225				
ATT	CCT	GGT	CTG	CTG	AAC	CAA	ACC	TCC	AGG	TCC	CTG	GAC	CAA	ATC	CCC	4048
Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	
	230					235					240					
GGA	TAC	CTG	AAC	AGG	ATA	CAC	GAA	CTC	TTG	AAT	GGA	ACT	CGT	GGA	CTC	4096
Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	
245					250					255					260	
TTT	CCT	GGA	CCC	TCA	CGC	AGG	ACC	CTA	GGA	GCC	CCG	GAC	ATT	TCC	TCA	4144
Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	
				265					270					275		
GGA	ACA	TCA	GAC	ACA	GGC	TCC	CTG	CCA	CCC	AAC	CTC	CAG	CCT	GGA	TAT	4192
Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	
			280					285					290			
TCT	CCT	TCC	CCA	ACC	CAT	CCT	CCT	ACT	GGA	CAG	TAT	ACG	CTC	TTC	CCT	4240
Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	
		295					300					305				
CTT	CCA	CCC	ACC	TTG	CCC	ACC	CCT	GTG	GTC	CAG	CTC	CAC	CCC	CTG	CTT	4288
Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	
	310					315					320					
CCT	GAC	CCT	TCT	GCT	CCA	ACG	CCC	ACC	CCT	ACC	AGC	CCT	CTT	CTA	AAC	4336
Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn	
325					330					335					340	

ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA GGG TAAGGTTCTC	4385
Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly	
345 350	
AGACACTGCC GACATCAGCA TTGTCTCGTG TACAGCTCCC TTCCCTGCAG GGC GCCCCTG	4445
GGAGACAACT GGACAAGATT TCCTACTTTC TCCTGAAACC CAAAGCCCTG GTAAAAGGGA	4505
TACACAGGAC TGAAAAGGGA ATCATTTTTTC ACTGTACATT ATAAACCTTC AGAAGCTATT	4565
TTTTTAAGCT ATCAGCAATA CTCATCAGAG CAGCTAGCTC TTTGGTCTAT TTTCTGCAGA	4625
AATTTGCAAC TCACTGATT CCAACATGCT CTTTTTCTGT GATAACTCTG CAAAGACCTG	4685
GGCTGGCCTG GCAGTTGAAC AGAGGGAGAG ACTAACCTTG AGTCAGAAAA CAGAGGAAGG	4745
GTAATTTCTT TTGCTTCAAA TTCAAGGCCT TCCAACGCCC CCATCCCCTT TACTATCATT	4805
CTCAGTGGGA CTCTGATC	4823

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Leu	Thr	Glu	Leu	Leu	Leu	Val	Val	Met	Leu	Leu	Leu	Thr	Ala
1				5					10					15	
Arg	Leu	Thr	Leu	Ser	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val
			20					25					30		
Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser
		35					40					45			
Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala
	50					55					60				



Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys
65					70					75					80
Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
			85						90					95	
Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly
			100					105					110		
Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu
		115					120					125			
Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp
	130						135					140			
Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val
145					150					155					160
Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala
			165						170					175	
Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu
			180					185					190		
Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr
		195					200					205			
Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly
		210				215					220				
Phe	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu
225					230					235					240
Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly
				245					250					255	
Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro
			260					265					270		
Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu
		275					280					285			
Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr
	290					295					300				

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
305 310 315 320

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
325 330 335

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
340 345 350

Gly